THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A method for identifying candidate genes capable of producing hybrid vigour in an animal or plant, comprising the steps of:

(i) comparing the nucleotide sequence of alleles of candidate genes isolated from an animal or plant which exhibits hybrid vigour with the nucleotide sequences from the corresponding alleles isolated from the parents of said animal or plant;

(ii) identifying nucleotide sequence differences in the alleles from said animal or plant which exhibits hybrid vigour which codes for amino acid sequence variation; and

(iii) identifying that the amino acid sequence variation between alleles of the candidate gene in said animal or plant is encoded by nucleotide sequences which are located within two or more different exons within the candidate gene.

2. A method according to claim 1, wherein the amino acid sequence variation is a conservative modified variation.

3. A method according to claim 1, wherein the amino acid sequence variation is a non-conservative modified variation.

4. A method according to claim 1, wherein the step of identifying the nucleotide sequence difference comprises the step of sequencing the nucleotide sequence isolated from said plant or animal.

5. A method according to claim 1, wherein the plant is selected from the group consisting of barley, rye, sorghum, maize, soybean, wheat, corn, potato, cotton, rice, oilseed rape (including canola), sunflower, alfalfa,

sugarcane, banana, blackberry, blueberry, strawberry, and raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits (such as apple, peach, pear, cherry and plum) and vegetable brassicas (such as broccoli, cabbage, cauliflower, brussel sprouts and kohlrabi). Other crops, fruits and vegetables whose phenotype may be changed include barley, currant, avocado, citrus fruits such as oranges, lemons, grapefruit and tangerines, artichoke, cherries, nuts such as the walnut and peanut, endive, leek, roots, such as arrowroot, beet, cassava, turnip, radish, yam, sweet potato and beans.

6. A method according to claim 1, wherein the animal is a mammal or fish.

7. A method according to claim 6, wherein the mammal is selected the mammalian Orders Primates, Rodentia, Lagomorpha, Cetacea, Carnivora, Perissodactyla and Artiodactyla.

8. A method according to claim 7, wherein the Artiodactyla is selected from one of the nine families, Suidae, Tayassuidae, Hippopotamidae, Camelidae, Tragulidae, Giraffidae, Cervidae, Antilocapridae and Bovidae.

9. A method according to claim 8, wherein the animal selected from Bovidae is an ungulate.

10. A method according to claim 9, wherein the ungulate is selected from the group consisting of cows or bulls, bison, buffalo, sheep, big-horn sheep, horses, ponies, donkeys, mule, deer, elk, caribou, goat, water buffalo, camels, llama, alpaca, and pigs.

11. A method according to claim 6, wherein the animal is a fish.

12. A method according to claim 11, wherein the fish is selected from the group consisting of zebrafish, European carp, salmon, mosquito fish, tench, lampreys, round gobies, tilapia and trout.

13. A method according to claim 8, wherein the animal is a human.

14. A method for identifying candidate genes capable of producing hybrid debility (HD) in an animal or plant, comprising the steps of:

(i) comparing the nucleotide sequence of alleles of candidate genes isolated from an animal or plant which exhibits said hybrid debility (HD) with the nucleotide sequences from the corresponding alleles isolated from the parents of said animal or plant;

(ii) identifying nucleotide sequence differences in the alleles from said animal or plant which exhibits said hybrid debility (HD) which codes for amino acid sequence variation; and

(iii) identifying that the amino acid sequence variation between alleles of the candidate gene in said animal or plant is encoded by nucleotide sequences which are located within two or more different exons within the candidate gene.

15. A method according to claim 14, wherein the amino acid sequence variation is a conservative modified variation.

16. A method according to claim 14, wherein the amino acid sequence variation is a non-conservative modified variation.

17. A method according to claim 14, wherein the step of identifying the nucleotide sequence difference comprises the step of sequencing the nucleotide sequence isolated from said plant or animal.

18. A method according to claim 14, wherein the plant is a weed or other noxious plant.

19. A method according to claim 14, wherein the animal is a pest.

20. A method according to claim 19, wherein the pest animal is a rodent, rabbit or fish.

21. A method for producing hybrid vigour or hybrid debility in an animal or plant, comprising the steps of:

(i) comparing the nucleotide sequence of alleles isolated from a gene from an animal or plant which promotes hybrid vigour or hybrid debility with the nucleotide sequences from the corresponding alleles isolated from the parents of said animal or plant;

(ii) identifying nucleotide sequence differences in the alleles from said animal or plant which promote hybrid vigour or hybrid debility which code for amino acid sequence variation; and

(iii) identifying that the amino acid sequence variation between alleles of the candidate gene in said animal or plant is encoded by nucleotide sequences which are located within two or more different exons within the candidate gene.

(iv) preparing a construct comprising nucleotide sequence from the alleles which promotes hybrid vigour or hybrid debility within said animal or plant;

(v) transforming said construct into a recipient plant or animal cell;

(vi) regenerating a plant or animal, which

expresses said construct, from said cell.

22. A method of detecting the presence or absence of hybrid mRNA in a plant or animal comprising the step of isolating mRNA from a plant or animal and comparing the nucleotide sequence of said mRNA to the corresponding coding sequence of the plant or animal's alleles.

23. A construct comprising a synthetic gene comprising exons from different alleles of a gene, wherein said alleles code for amino acid sequence variation wherein the variation occurs between different alleles.

24. Use of hybrid mRNA molecules produced in vitro or in vivo to overcome hybrid debility in a plant or animal and/or induce hybrid vigour in a plant or animal comprising the step of introducing said hybrid mRNA into said animal or plant.

25. Use according to claim 24, wherein the step of introducing said hybrid mRNA into said animal or plant is by transformation.

26. Use according to claim 25, wherein the step of transformation into a plant is selected from the group consisting of homologous recombination, microprojectile bombardment, PEG mediated transformation, electroporation, silicon carbide fibre mediated transformation, or Agrobacterium-mediated transformation.

27. A method for producing genetically engineered or transgenic non-human animal by inserting a synthetic gene into a non-human somatic cell or cell nucleus prior to transferring the somatic cell or cell nucleus, wherein said synthetic gene comprises exons from different alleles of a gene, wherein said alleles code for amino acid sequence variation, wherein the variation does not occur

in the same allele.

28. A genetically engineered or transgenic animal obtained by a method according to claim 27.

29. A method according to claim 27, wherein the animal cells are isolated from a mammal and fish.